

IN THE SPECIFICATION:

In the first line of the specification following the title, please insert the following paragraph:

This application claims the benefit of U.S. provisional application Serial No. 60/151,494, filed August 30, 1999.

IN THE CLAIMS:

Please enter the following amended claim set:

Please cancel Claims 1-11 and 23-45 without prejudice to filing claims of similar scope in a continuing or divisional application.

1. (Amended) A method for analyzing a nucleic acid sample comprising three or more loci each having at least two different allelic sequences, said method comprising:
- (a) combining at least a first, a second and a third pair of oligonucleotide probes with said nucleic acid, each of the members of said pairs being capable of hybridizing in proximity to each other to a segment of said nucleic acid comprising at least one of ~~said~~ ~~multiple loci~~ ^{said three or more loci}, wherein (i) the first member of each pair comprises a FRET donor and the second member comprises a FRET acceptor, wherein the FRET acceptor of the second member in said first pair has an emission spectrum which is different from the emission spectrum of the FRET acceptor of said second and third oligonucleotide probe pairs, (ii) when said second and third probe pairs have the same FRET acceptor, each of said second and third probe pairs has a different T_m from each other for each different allele within the nucleic acid segment to which each member hybridizes (iii) upon hybridization, the proximity of the members of a probe pair is sufficient to allow fluorescence resonance energy transfer between said FRET donor and said FRET acceptor, and (iv) at least one of said members of each pair has a sequence which results in the differential hybridization of that member with at least two different alleles which may be present at said loci;
- (b) measuring the emission of each of said FRET acceptors at a first temperature;
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